

Fig 1

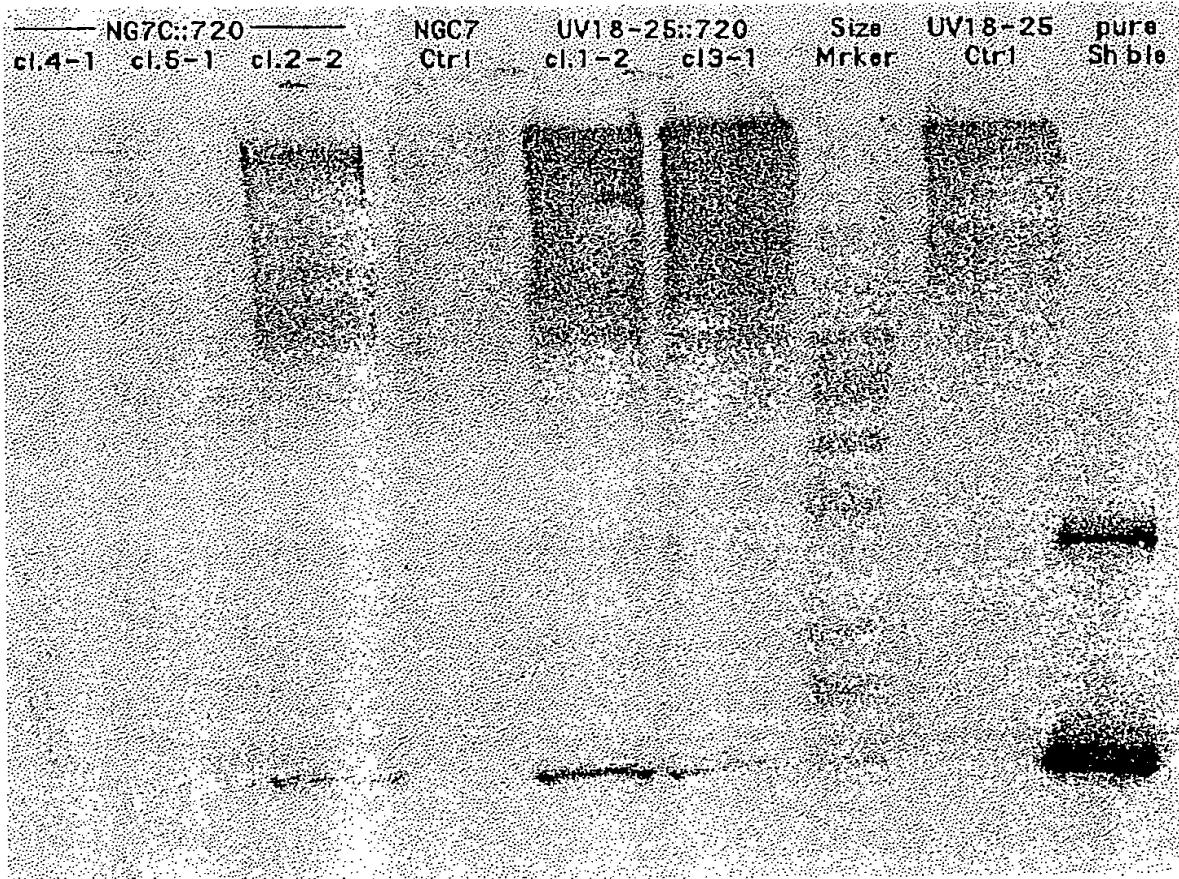


Fig 2

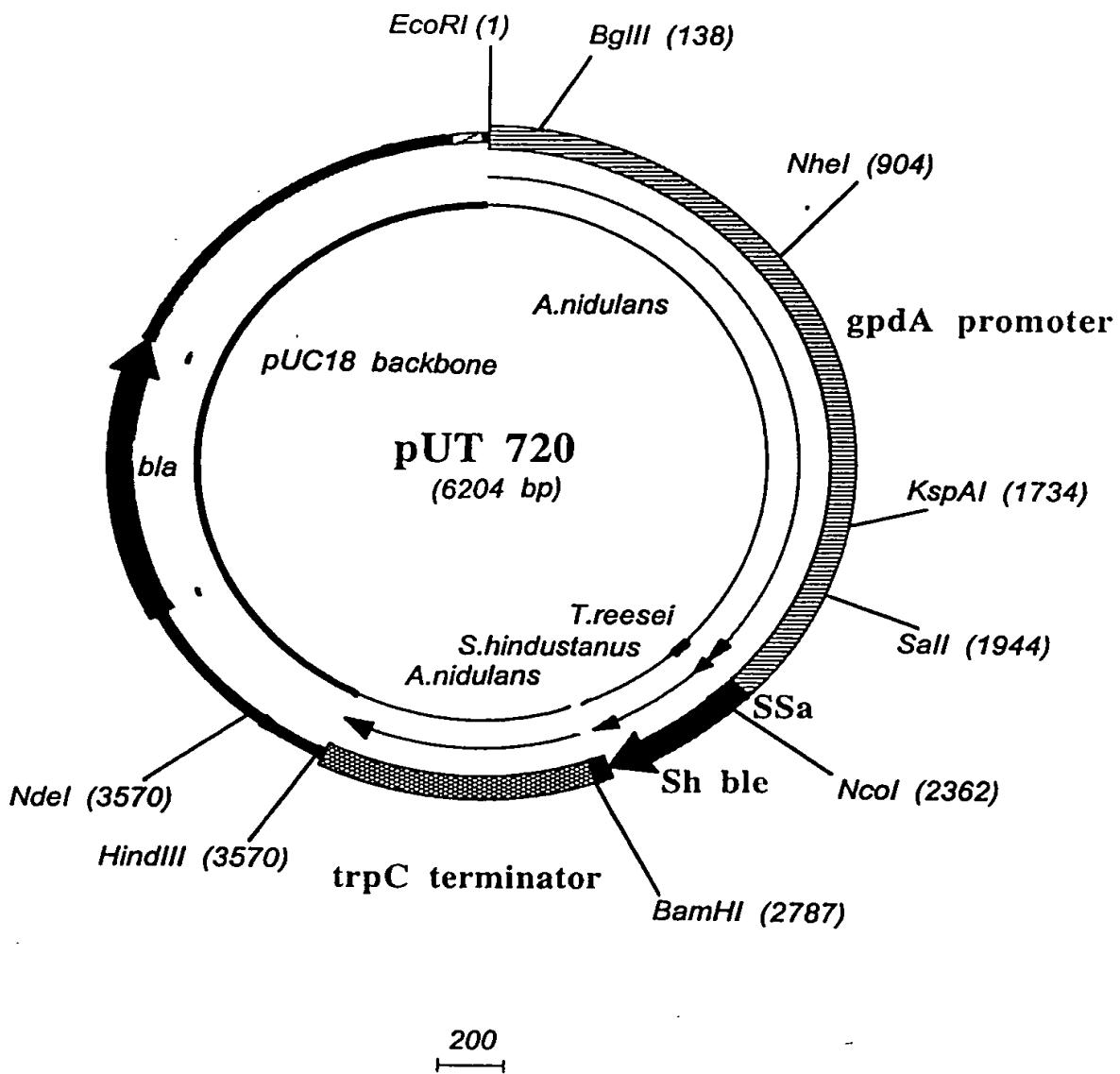


Fig 3

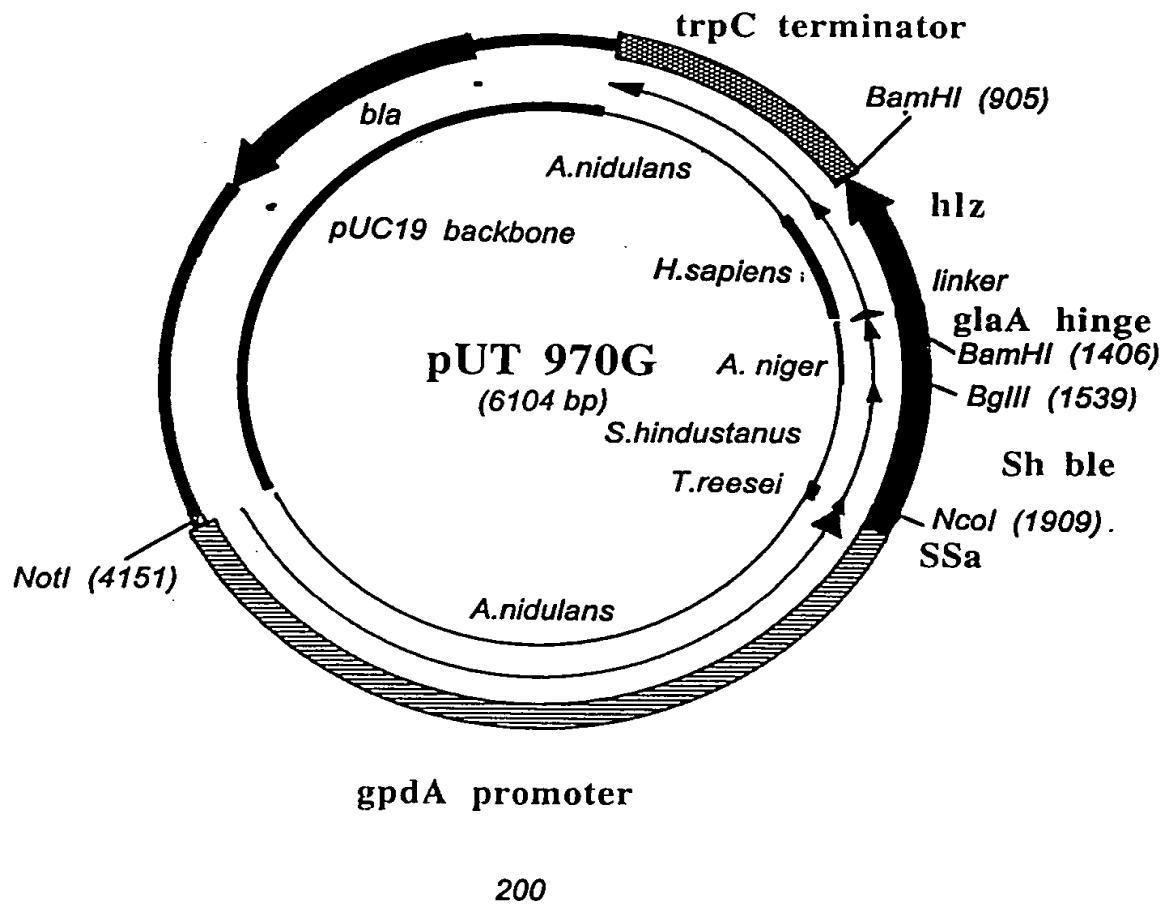


Fig 4

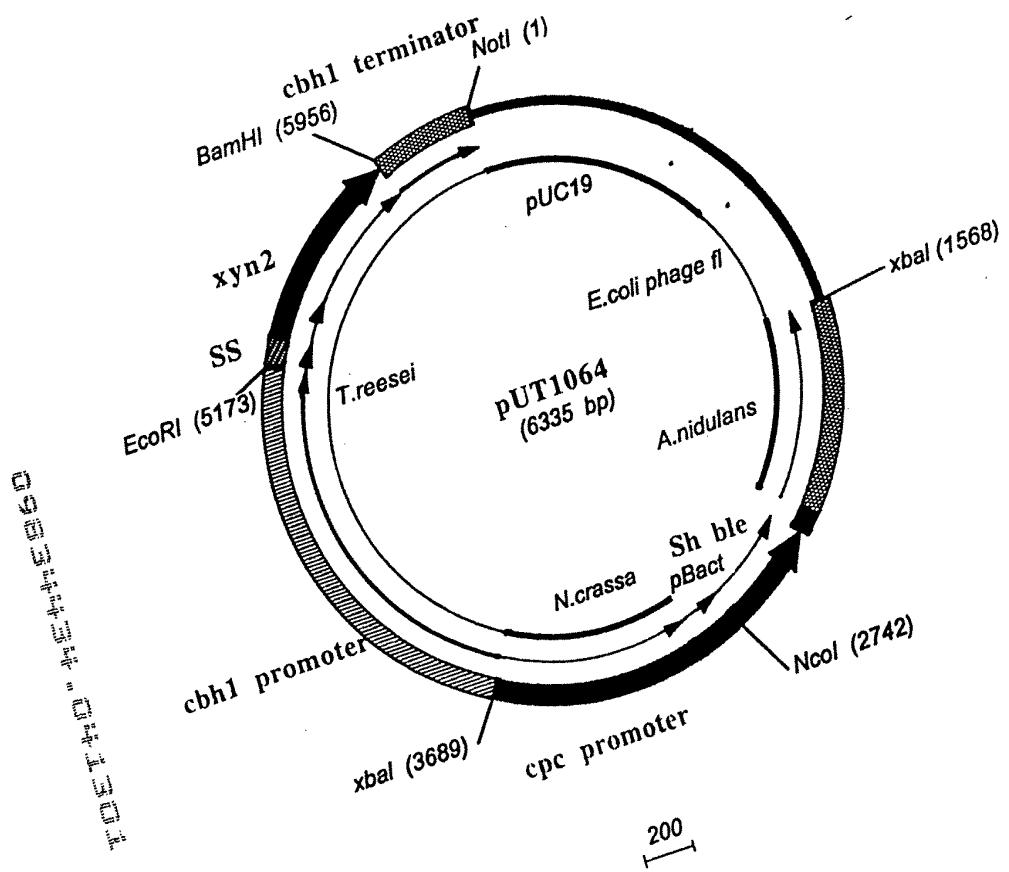
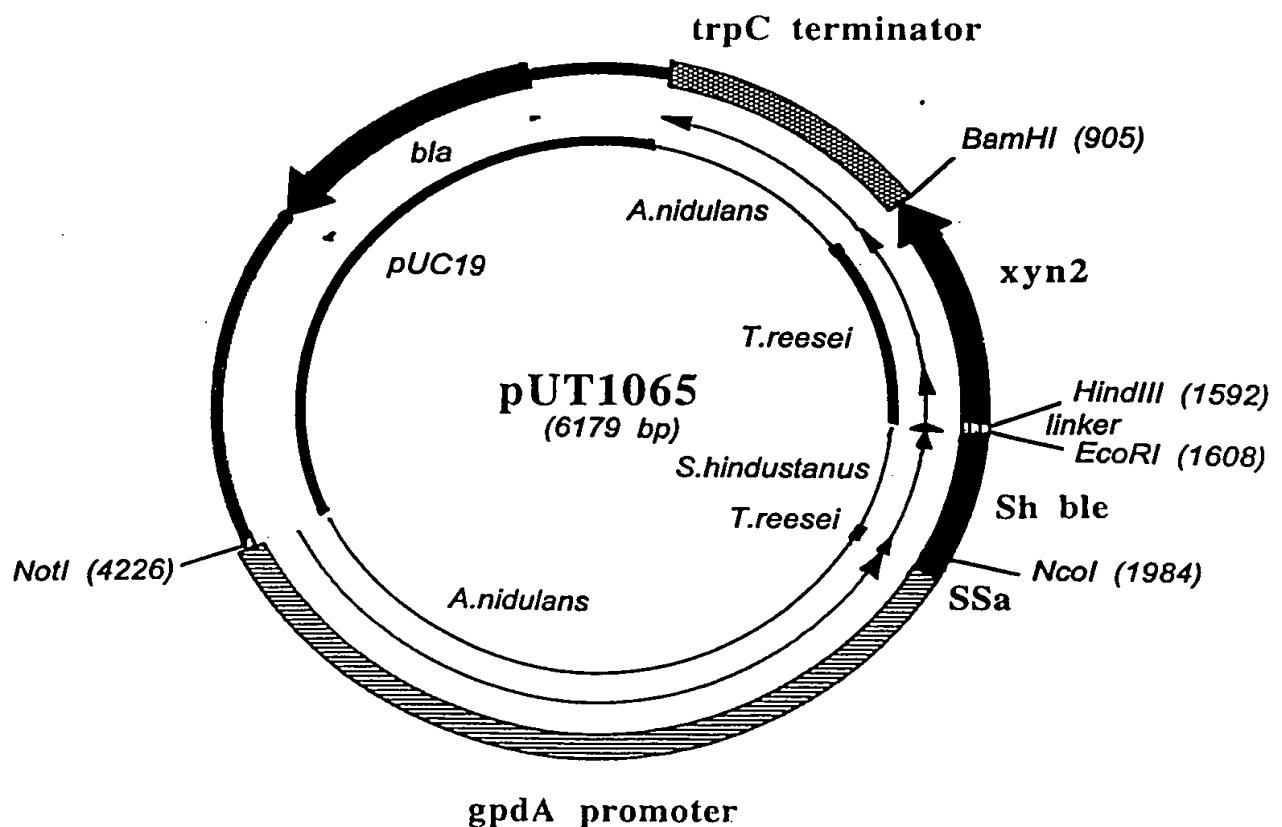


Fig 5



200

Fig 6

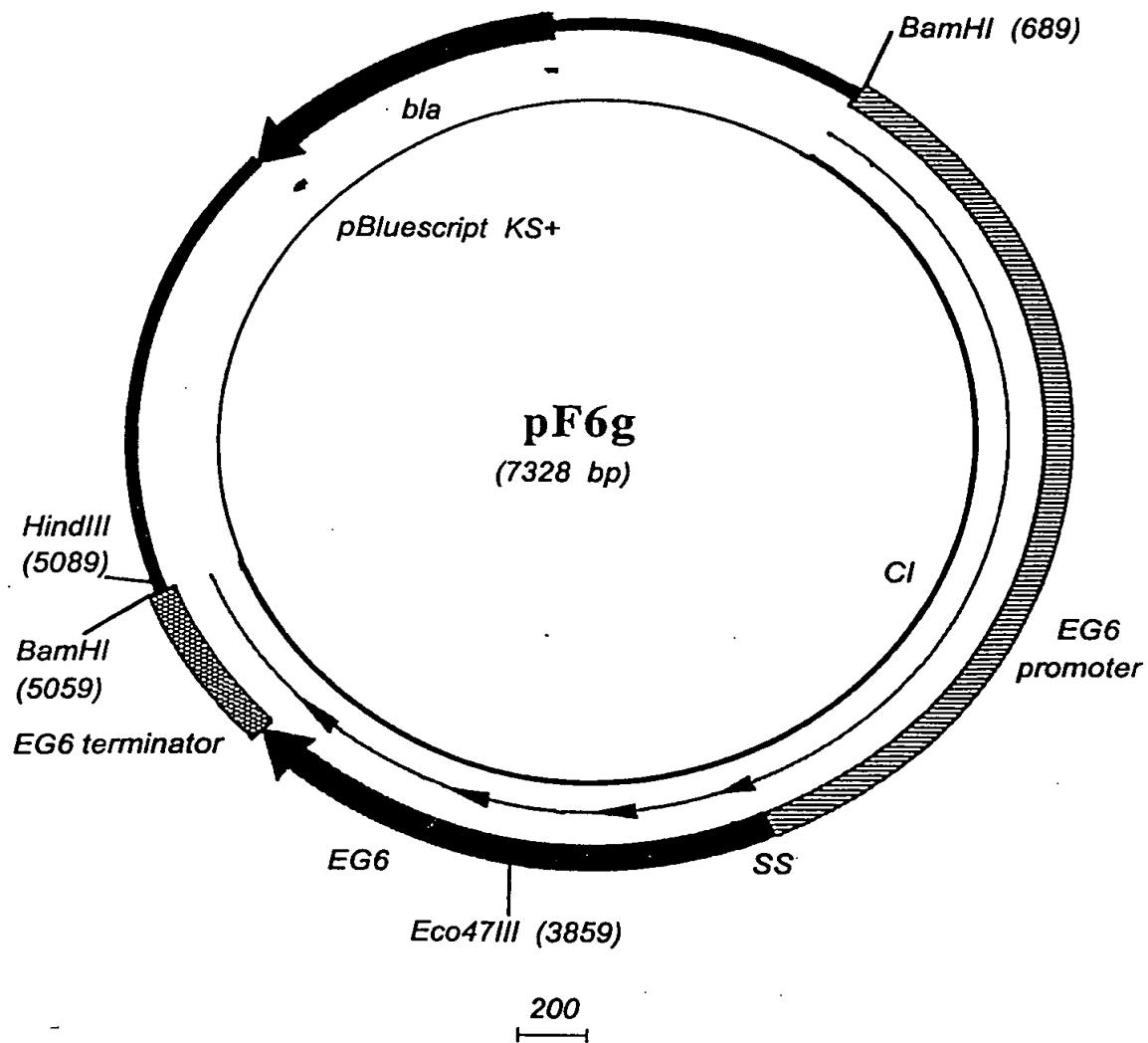
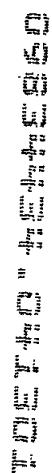


Fig 7

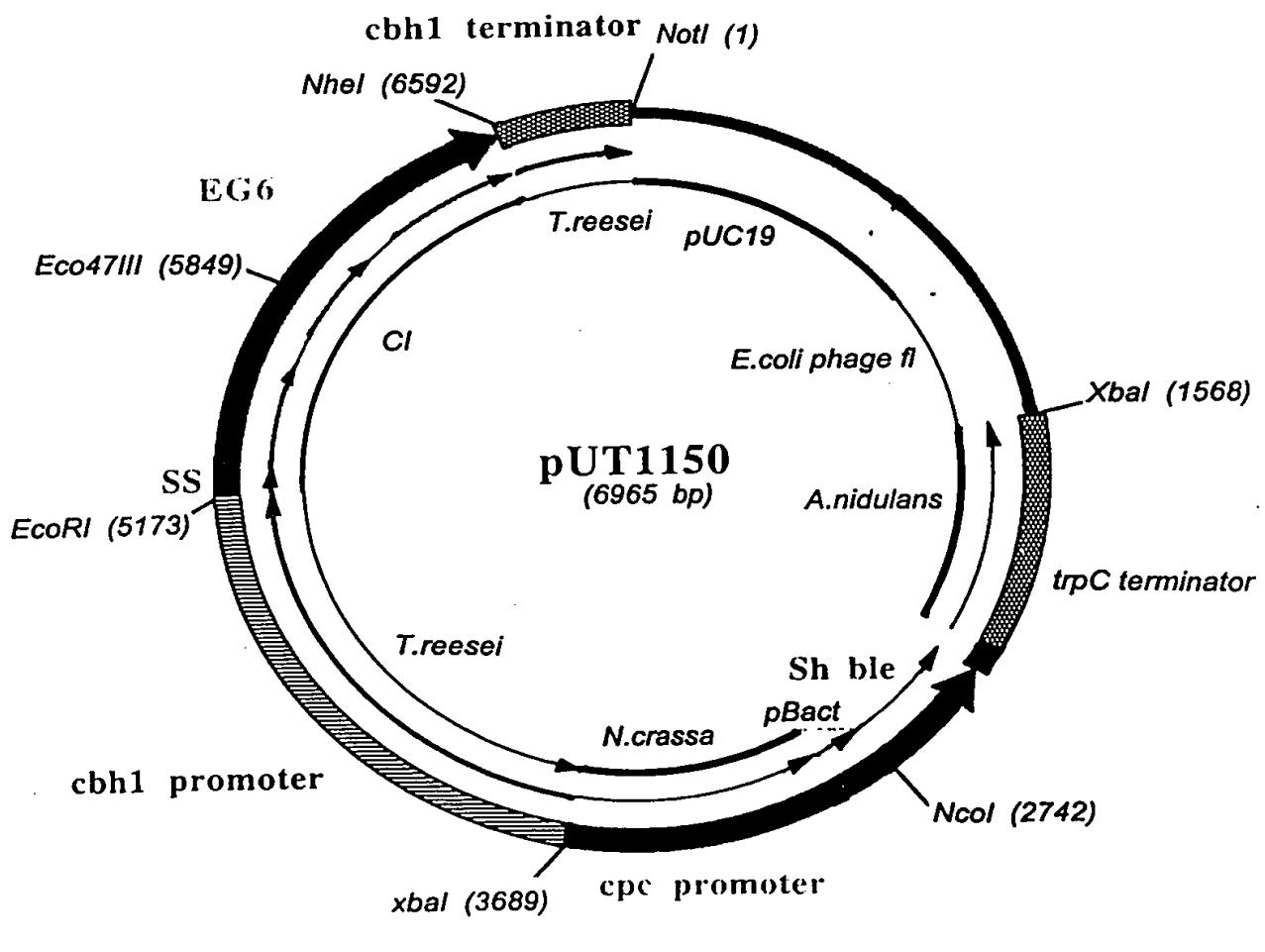


Fig 8

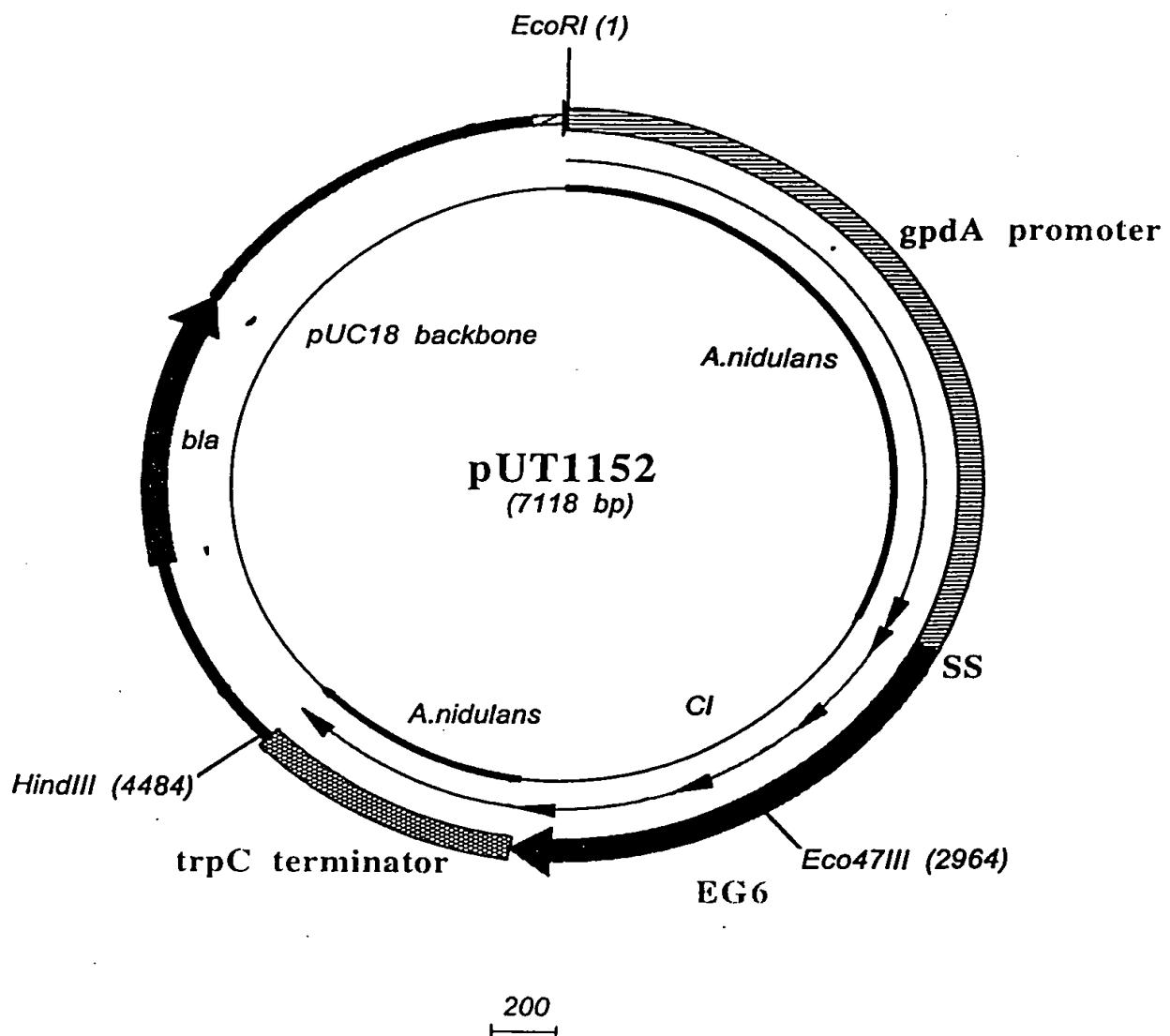


Fig 9

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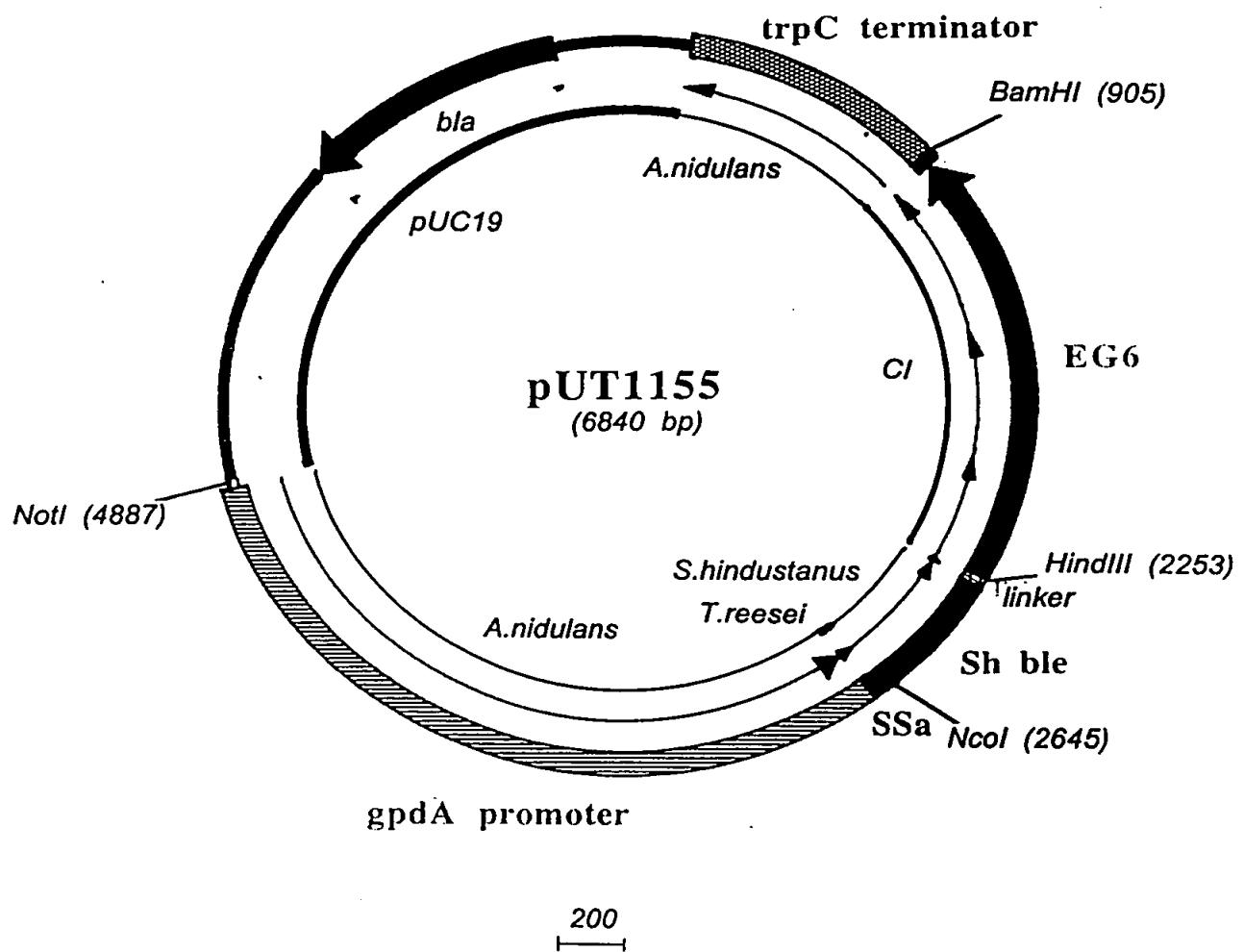


Fig 10

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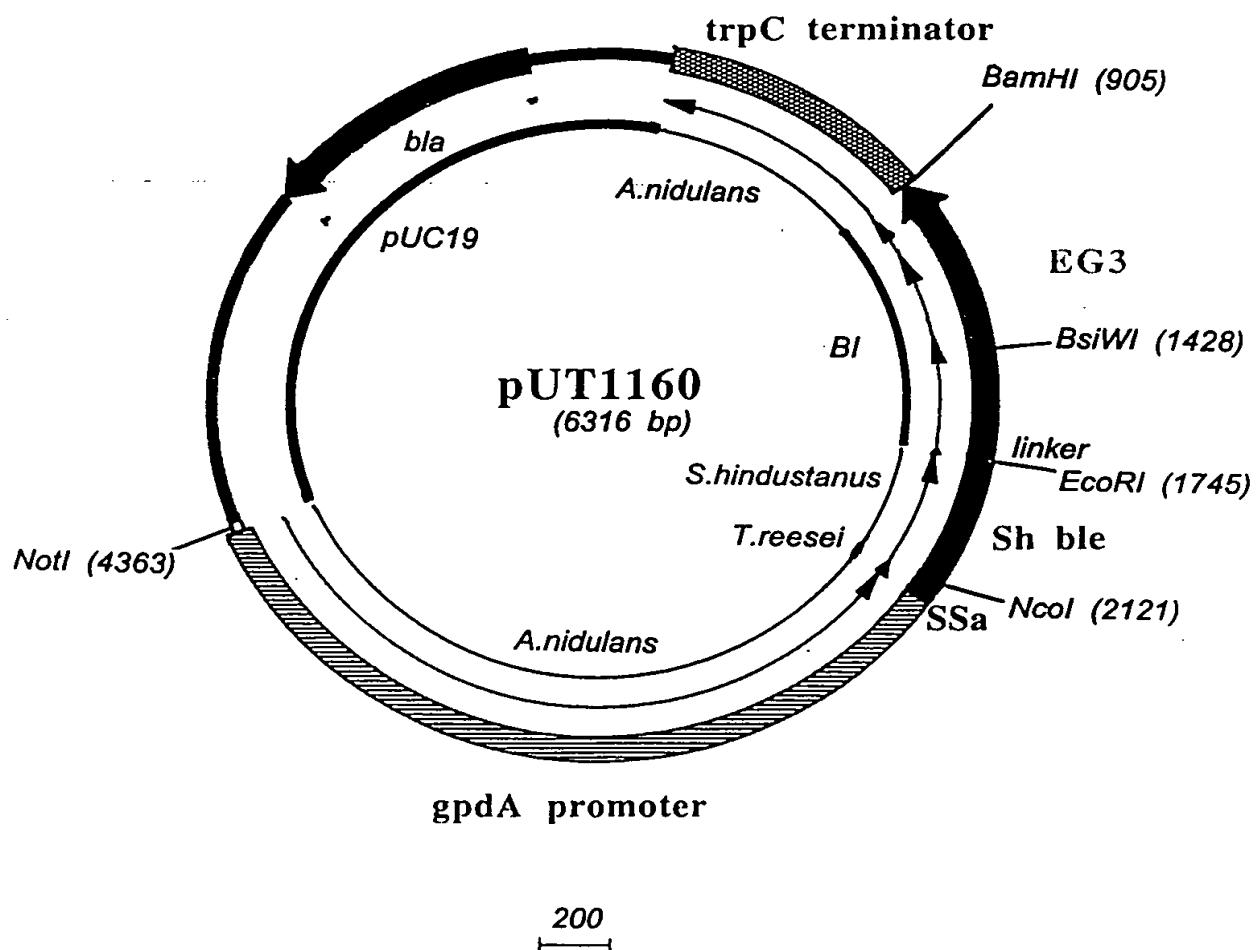
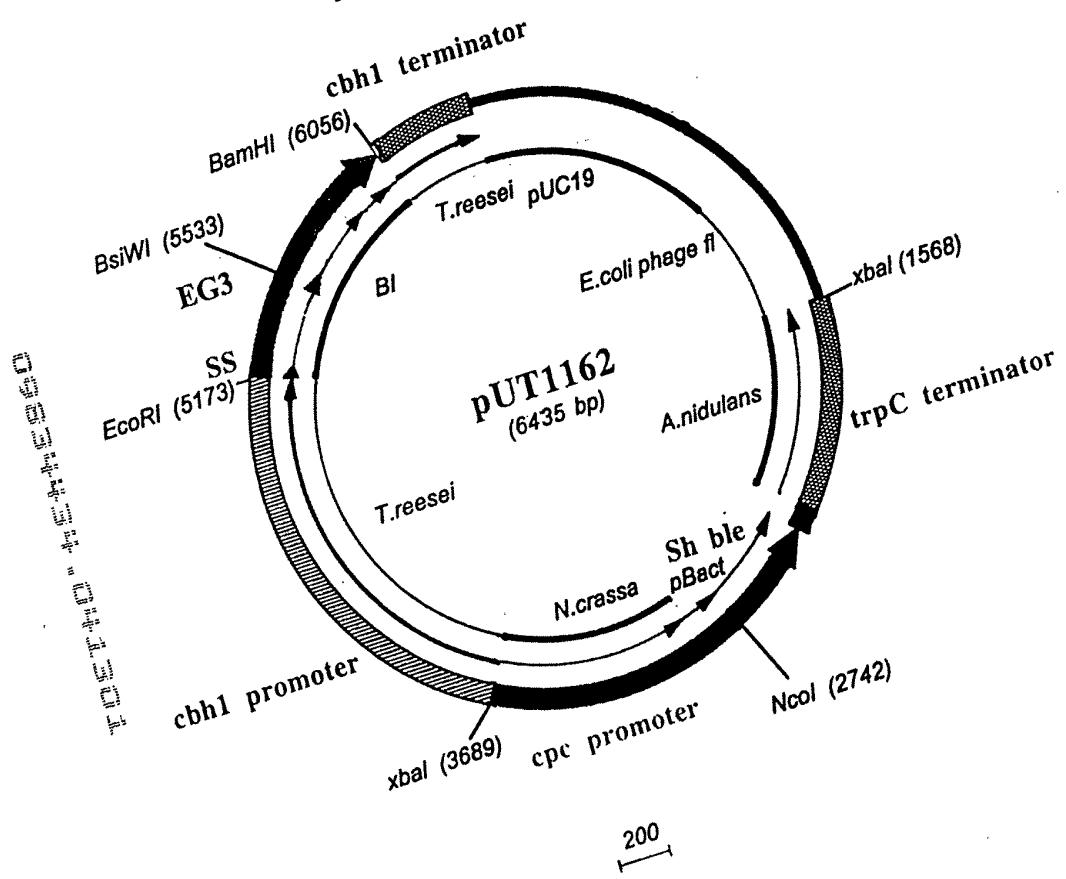


Fig 11



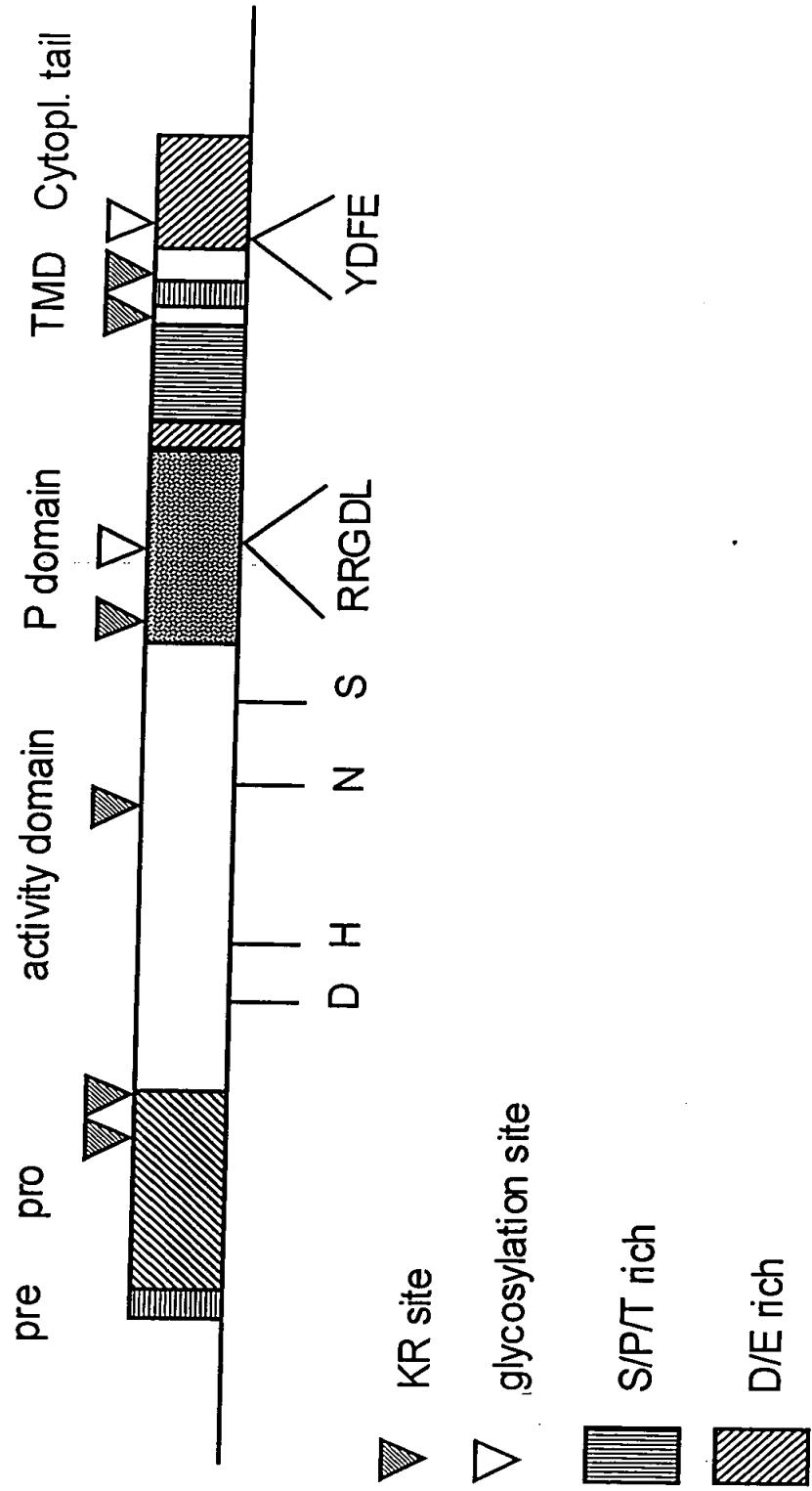


Fig 12

Fig 13B

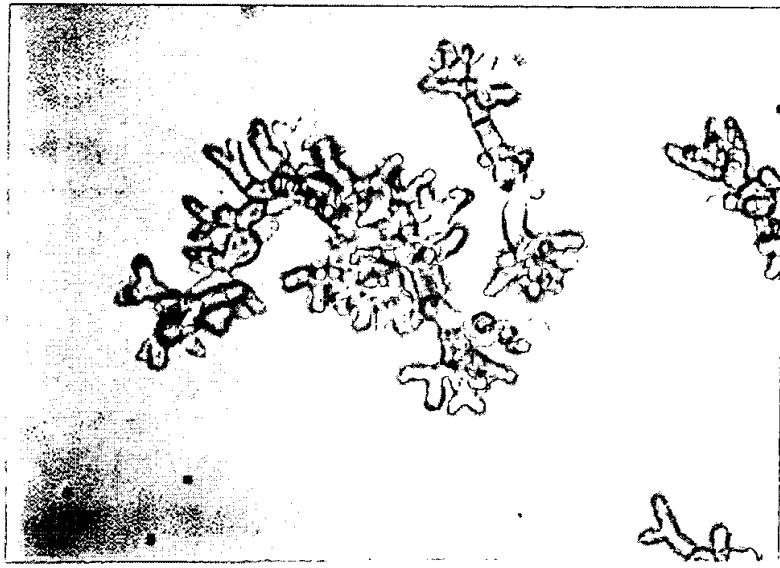
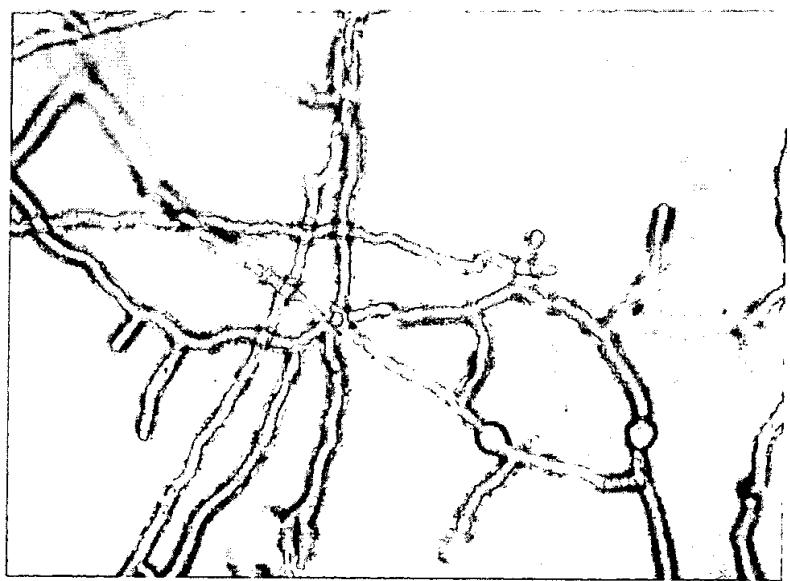


Fig 13A



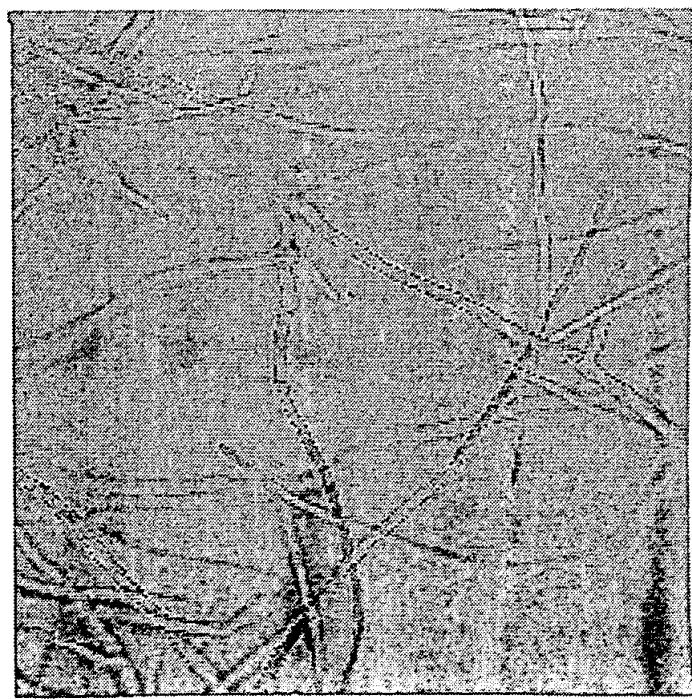


Fig. 14A

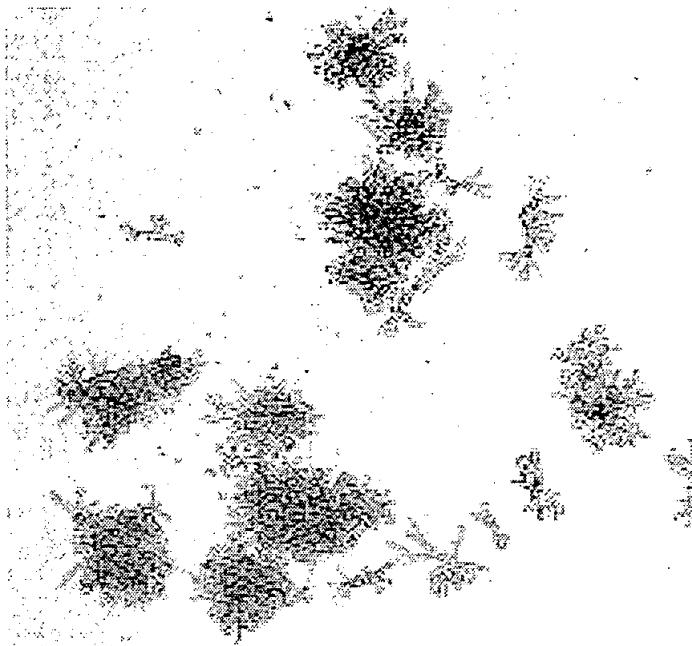


Fig. 14B

pyrE gene sequence

SEQ ID NO:1

Pyre/niger Length: 1578 March 9, 2001 09:28 Type: N Check: 2282

1 GGGTTAATGT GAAGGCGTTA GTGGTAATGT ATATTAATGG TGAGATGGC
51 TTTGATTGGG TTTAATTGGA ATCTGTATAT TTTCAGATGG AGTCAACTTT
101 TGAATGGCCA ATATATCCTC GGCGATACCG TCGGAGATAA GATAAGAATA
151 ATCGCACACT ATTCCCAAAG CATACTGGTA CATACTGCAT TCGGCTAGTG
201 CGGGGTGCTT ACCTCATCCA CCCGAATGAG CCCAACTTTT TTGTCTCAAT
251 CAATAATTGC ATCCAAATTC CCCCAGCAACT TCCCCCTCCA ACCCCGTGTC
301 TATACCACTC CCTCCACACC CACACAATCA CAATGGCTCT CCCTGCCTAC
351 AAGACCGCCT TCCTGGAGTC TCTCGTCGGC CAACGTGCTG ACTTTCGGCA
401 CCTTCACCCT GAAGTCGGGT CGCCGTGCGT CACCCCTCCA ACACCGGCAT
451 TATCGCAATC GGAAGACTTA CCACTGTATA CAGACTCCCC CTACTTCTTC
501 AACGCCGGCA TCTTCAACAC CGCCTCTCTC CTCTCCGCC TCTCCACCAT
551 GGCCCACACC ATCATCACCT TCCTCGCTGA GAACCCTTCC ATCCCCAAGC
601 CCGACGTCAT GCTTCGGGTA AAAAACCCCC TCTTCCCCA ATACCCCACT
651 TCCACTCAAC AACCCATAAA TAACTAACAA AAACCCCTA AACAGCCCCG
701 CATACAAAGG CATCCCCCTC GCGTGCGCCA CCCTCCTTGA ACTCAACCGC
751 ATCGACCCCG CCACCTGGGG CAGCGTGTCC TACAGCTACA ACCGCAAAGA
801 AGCCAAGGAT CACGGCGAAG GCGGCAACAT TGTCGGCGCC GCTCTGAAGG
851 GCAAGACCGT GCTTGTGATC GACGATGTCA TCACGGCCGG TACCGCCATG
901 CGTGAGACCC TCAACCTGGT CGCCAAGGAG GCGGGCAAGG TCGTCGGATT
951 CACTGTTGCT CTGGACCGCT TGGAGAAGAT GCCCGGACCC AAGGACGAGA
1001 ACGGTGTCGA GGACGATAAG CCCAGAATGA GTGCTATGGG TCAGATCCGT
1051 AAGGAGTATG GTGTGCCAC GACGAGTATT GTTACTCTGG ATGATTGAT
1101 CAAGTTGATG CAGGCGAAGG GCAATGAGGC CGATATGAAG CGGTTGGAGG
1151 AGTATAGGGC TAAGTATCAG GCTAGTGATT AGTCGGTTTC ATTGACCGAT

FIG. 15A

1201 TGTTTGGGTG GGTGTGAGAG GTTAGGTTAG GTTGTGGCG TAGGAATGAA
 1251 AAGCTGTATA CATAGGGGCC TGAAGAGGTG CGTAGAGACG GTCGTGAGAT
 1301 GTTTTATGTC AAAATCTTGA ACAAAATGACA CCTTAAAAAA GACCCCTTGG
 1351 TTTCAAGCTGA ATTAGCCCGG AAAGATGCTC GGCACGCCAT GAGTCTAGCC
 1401 CACTCAGTGG GCACCCGTT CCCACATTG AAGTGGCCGA CGCTTATTG
 1451 GCTGAGGCTG TGGCCTGGAA AGGCACATATG GCGTGCTGCG GTACAAGGCC
 1501 GGGGCTGGCG TACGAACCAC GACGCCGAA GGGAACTCTT CGGTCTTACT
 1551 ACTACTATGT CCCCCAGTTGA CCCCCCGA

SEQ ID NO:2

Translation of pyrE(1-1578)
 Universal code

1 GGGTTAACGTGAAGGCCTTAGTGGTAATGTATATTAAATGGTGGAGATGGGCTTGATTGGG
 CCCAATTACACTTCCGCAATCACCATTACATATAATTACCACTCTACCCGAAACTAACCC
 1 G L M * R R * W * C I L M V R W A L I G
 1 G * C E G V S G N V Y * W * D G L * L G
 1 V N V K A L V V M Y I N G E M G F D W V

61 TTTAATTGGAATCTGTATATTTCAAGATGGAGTCAACTTGAATGCCAATATATCCTC
 AAATTAACCTTAGACATATAAAAGTCTACCTCAGTGAAAACCTACCGTTATAGGAG
 21 F N W N L Y I F R W S Q L L N G Q Y I L
 21 L I G I C I F S D G V N F * M A N I S S
 21 * L E S V Y F Q M E S T F E W P I Y P R

121 GGCGATACCGTCGGAGATAAGATAAGATAATCGCACACTATTCCAAAGCATACTGGTA
 CCGCTATGGCAGCCTCTATTCTATTAGCGTGTGATAAGGGTTCGTATGACCAT
 41 G D T V G D K I R I I A H Y S Q S I L V
 41 A I P S E I R * E * S H T I P K A Y W Y
 41 R Y R R R * D K N N R T L F P K H T G T

181 CATACTGCATCGGCTAGTGCAGGGGTGCTTACCTCATCCACCCGAATGAGCCAACTTTT
 GTATGACGTAAGCCGATCACGCCACGAATGGAGTAGGTGGCTTACTCGGGTTGAAAA
 61 H T A F G * C G V L T S S T R M S P T F
 61 I L H S A S A G C L P H P P E * A Q L F
 61 Y C I R L V R G A Y L I H P N E P N F F

FIG. 15B

卷之三

241 TTGTCTCAATCAATAATTGCATCCAAATTCCCCCGCAACTTCCCCCTCCAACCCCGTGTCAACAGAGTTAGTTAACGTAGGTTAAGGGGGCGTTGAAGGGGGAGGTTGGGCACAG

81 L S Q S I I A S K F P R N F P L Q P R V
81 C L N Q * L H P N S P A T S P S N P V S
81 V S I N N C I Q I P P Q L P P P T P C L
????????????

301 TATACCACTCCCTCACACCCACACAATCACAATGGCTCTCCCTGCCTACAAAGACCGCCTATATGGTGAGGGAGGTGTGGGTGTAGTGTACCGAGAGGGACGGATGTTCTGGCGGA

101 Y T T P S T P T Q S Q W L S L P T R P P
101 I P L P P H P H N H N G S P C L Q D R L
101 Y H S L H T H T I T M A L P A Y K T A F

361 TCCTGGAGTCTCGTCGGCCAACGTGCTGACTTTCGGCACCTCACCCCTGAAGTCGGGT
AGGACCTCAGAGAGCAGCCGGTTGCACGACTGAAAGCCGTGGAAGTGGACTTCAGCCCA
????????????????????????

121 S W S L S S A N V L T F G T F T L K S G
121 P G V S R R P T C * L S A P S P * S R V
121 L E S L V G Q R A D F R H L H P E V G S

421 INTRON I
CGCCGTGCGTCACCCCTCCAACACCGGCATTATCGCAATCGGAAGACTTACCACTGTATA
GCGGCACGCAGTGGGGAGGTTGTGGCCGTAATAGCGTTAGCCTCTGAATGGTGACATAT

141 R R A S P L Q H R H Y R N R K T Y H C I
141 A V R H P S N T G I I A I G R L T T V Y
141 P C V T P P T P A L S Q S E D L P L Y T

481 CAGACTCCCCCTACTTCTTCAACGCCGGCATCTTCAACACCGCCTCTCTCTCCGCC
GTCTGAGGGGGATGAAGAAGTTGCGGCCGTAGAAGTTGTGGCGGAGAGAGGAGAGGCCGG

161 Q T P P T S S T P A S S T P P L S S P P
161 R L P L L L Q R R H L Q H R L S P L R P
161 D S P Y F F N A G I F N T A S L L S A L

541 *NcoI*
TCTCCACCATGGCCCACACCATCATCACCTTCCCTCGCTGAGAACCCCTCCATCCCCAAGC
AGAGGTGGTACCGGGTGTGGTAGTAGTGGAAAGGAGCGACTCTGGGAAGGTAGGGTTCG

181 S P P W P T P S S P S S L R T L P S P S
181 L H H G P H H H H L P R * E P F H P Q A
181 S T M A H T I I T F L A E N P S I P K P
????????????

601 INTRON II
CCGACGTCATGCTTGGGTAAAAACCCCTCTTCCCCAATACCCACTCCACTCAAC
GGCTGCAGTACGAAGCCCATTGGGGAGAAAGGGTTATGGGTGAAGGTGAGTTG

201 P T S C F G * K T P S F P N T P L P L N
201 R R H A S G K K P P L S P I P H F H S T
201 D V M L R V K N P L F P Q Y P T S T Q Q

FIG. 15C

TaqI PstI SphI SalI KpnI

661 AACCCATAAATAACTAACAAAAACCCCTAAACAGCCCCGATACAAAGGCATCCCCCTC
TTGGGTATTATTGATTGTTTGGGGATTGTCGGGCGTATGTTCCTAGGGGGAG

221 N P * I T N K N P L N S P A Y K G I P L
221 T H K * L T K T P * T A P H T K A S P S
221 P I N N * Q K P P K Q P R I Q R H P P R

721 GCGTGCGCCACCCCTCTGAACCTAACCGCATCGACCCGCCACCTGGGCAGCGTGTCC
CGCACGCGTGGGAGGAACCTGAGTTGGCGTAGCTGGGCGGTGGACCCGTCGCACAGG

241 A C A T L L E L N R I D P A T W G S V S
241 R A P P S L N S T A S T P P P P G A A A C P
241 V R H P P * T Q P H R P R H L G Q R V L

781 TACAGCTACAACCGCAAAGAACCCAAGGATCACGGCAAGGCCAACATTGTCGGGCC
ATGTCGATGTTGGCGTTCTTCGGTTCTAGTGCCGTTCCGCTGTAAACAGCCGCGG

261 Y S Y N R K E A K D H G E G G N I V G A
261 T A T T A K K P R I T A K A A T L S A P
261 Q L Q P Q R S Q G S R R R Q H C R R R

841 *KpnI*
GCTCTGAAGGGCAAGACCGTGCTTGTGATCGACGATGTCATCACGGCCGGTACCGCCATG
CGAGACTTCCCCTGGCACGAACACTAGCTGCTACAGTAGTGCCTGGCCATGGCGGTAC

281 A L K G K T V L V I D D V I T A G T A M
281 L * R A R P C L * S T M S S R P V P P C
281 S E G Q D R A C D R R C H H G R Y R H A

901 CGTGAGACCTCAACCTGGTCGCCAAGGAGGGCGCAAGGTCGTCGGATTCACTGTTGCT
GCACTCTGGAGTTGGACCAGCGGTTCCCTCCGCCAGCAGCTAACGTGACAACGA

301 R E T L N L V A K E G G K V V G F T V A
301 V R P S T W S P R R A A R S S D S L L L
301 * D P Q P G R Q G G R Q G R R I H C C C S

961 CTGGACCGCTTGGAGAAGATGCCGGACCAAGGACGAGAACGGTGTGAGGACGATAAG
GACCTGGCGAACCTCTTCTACGGGCTGGGTTCTGCTCTGCCACAGCTCCTGCTATTG

321 L D R L E K M P G P K D E N G V E D D K
321 W T A W R R C P D P R T R T V S R T I S
321 G P L G E D A R T Q G R E R C R G R * A

1021 CCCAGAATGAGTGCTATGGGTCAAGATCCGTAAGGAGTATGGTGTGCCACGACGAGTATT
GGGTCTTACTCACGATACCCAGTCTAGGCATTCTCATACACACGGGTGCTGCTCATAA

341 P R M S A M G Q I R K E Y G V P T T S I
341 P E * V L W V R S V R S M V C P R R V L
341 Q N E C Y G S D P * G V W C A H D E Y C

FIG. 15D

1081 GTTACTCTGGATGATTGATCAAGTTGATGCAGGCGAAGGGCAATGAGGCCGATATGAAG
CAATGAGACCTACTAAACTAGTTCAACTACGTCCGCTTCCCGTTACTCCGGCTATACTTC

361 V T L D D L I K L M Q A K G N E A D M K
361 L L W M I * S S * C R R R A M R P I * S
361 Y S G * F D Q V D A G E G Q * G R Y E A

1141 CGGTTGGAGGAGTATAGGGCTAAGTATCAGGCTAGTGATTAGTCGGTTTCATTGACCGAT
GCCAACCTCCTCATATCCCGATTCAAGTCCGATCACTAATCAGCCAAAGTAACGGCTA

381 R L E E Y R A K Y Q A S D * S V S L T D
381 G W R S I G L S I R L V I S R F H * P I
381 V G G V * G * V S G * * L V G F I D R L

1201 TGTGGGGGTGGGTGTGAGAGGTTAGGTTAGGTTGGGCGTAGGAATGAAAAGCTGTATA
ACAAACCCACCCACACTCTCCAATCCAACACCCGCATCCTACTTTGACATAT

401 C L G G C E R L G * V V G V G M K S C I
401 V W V G V R G * V R L W A * E * K A V Y
401 F G W V * E V R L G C G R R N E K L Y T

1261 CATAGGGGCCTGAAGAGGGTGCCTAGAGACGGTCGTGAGATGTTTATGTCAAAATCTTGA
GTATCCCCGGACTTCTCCACGCATCTGCCAGCACTACAAAATACAGTTTAGAACT

421 H R G L K R C V E T V V R C F M S K S *
421 I G A * R G A * R R S * D V L C Q N L E
421 * G P E E V R R D G R E M F Y V K I L N

1321 ACAAAATGACACCTTAAAAAAGACCCCTTGGTTCACTGAATTAGCCCGAAAGATGCTC
TGTTTACTGTGGAATTCTGGGAACCAAGTCGACTTAATCGGGCTTCTACGAG

441 T N D T L K K T P W F Q L N * P G K M L
441 Q M T P * K R P L G F S * I S P E R C S
441 K * H L K K D P L V S A E L A R K D A R

1381 GGCACGCCATGAGTCTAGCCCACTCAGTGGGCACCCGTTCCACATTGAAGTGGCCGA
CCGTGCGGTACTCAGATCGGGTGAGTCACCCGTGGCAAAGGGTGTAAACTTCACCGGCT

461 G T P * V * P T Q W A P V S H I * S G R
461 A R H E S S P L S G H P F P T F E V A D
461 H A M S L A H S V G T R F P H L K W P T

1441 CGCTTATTTGGCTGAGGCTGTGGCCTGGAAAGGCACATGGCGTGCTGCCGTACAAGGCC
GCGAATAAACCGACTCCGACACCGGACCTTCCGTGATACCGCACGACGCCATGTTCCGG

481 R L F G * G C G L E R H Y G V L R Y K A
481 A Y L A E A V A W K G T M A C C G T R P
481 L I W L R L W P G K A L W R A A V Q G R

FIG. 15E

1501 GGGGCTGGCGTACGAACCACGACGCCGAAGGGAACTCTTCGGTCTTACTACTATGT
CCCCGACCGCATGCTTGGTGTGCGGGCTTCCCTTGAGAAGCCAGAATGATGATGATACA

501 G A G V R T T P E G N S S V L L L L L C
501 G L A Y E P R R P K G T L R S Y Y Y Y V
501 G W R T N H D A R R E L F G L T T T M S

1561 CCCCAGTTGACCCCCCGA
GGGGTCAACTGGGGGGCT

521 P Q L T P R
521 P S * P P
521 P V D P P